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AB It has been demonstrated that following prolonged treatment with reverse transcriptase inhibitors, especially with nucleoside analogs, resistant viral strains appear that show mutations in the nucleotides of the gene that codifies reverse transcriptase. These mutations cause changes in amino acids, which gradually increases resistance. In this study we evaluated the applicability of the LiPA HIV-1 RT test in determining the presence of mutations in this gene that can lead to resistance to antiretroviral treatments. Twenty-one samples were studied without previous knowledge of the antiviral treatments that the patients had received. No mutations in the HIV-1 strains from untreated patients were found. In the other patients who had undergone various treatment regimens, the results obtained with the LiPA HIV-1 RT made it possible to retrospectively identify the different nucleoside analogs they had been treated with. The most frequently found mutations were those that lead to a certain degree of resistance to AZT, followed by those related to resistance to ddI, which in effect in this order were the drugs used in the treatment of the patients. However, the LiPA HIV-1 RT test has certain limitations. It can only detect mutations that can be recognized by its sequences. As such, including sequences that would make it possible to study the possible genotypic variations in the gene that codifies the protease of HIV-1 would be helpful, given the importance of the protease inhibitors in clinical practice. In any case, direct sequencing continues to be standard method as it allows us to obtain full information on the genes that need to be studied.